IN VIVO VALIDATION OF PREDICTED AND CONSERVED T CELL EPITOPES IN A SWINE INFLUENZA MODEL

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Key Words: T cell epitope prediction, immunoinformatics, swine vaccine, immunogenicity, influenza, PigMatrix

Swine influenza is a highly contagious respiratory viral infection in pigs that is responsible for significant financial losses to pig farmers annually. Current measures to protect herds from infection include: inactivated whole-virus vaccines, subunit vaccines, and alpha replicon-based vaccines. As is true for influenza vaccines for humans, these strategies do not provide broad protection against the diverse strains of influenza A virus (IAV) currently circulating in U.S. swine. Improved approaches to developing swine influenza vaccines are needed. Here, we used immunoinformatics tools to identify class I and II T cell epitopes highly conserved in seven representative strains of IAV in U.S. swine and predicted to bind to Swine Leukocyte Antigen (SLA) alleles prevalent in commercial swine. Epitope-specific interferon-gamma (IFN□) recall responses to pooled peptides and whole virus were detected in pigs immunized with multi-epitope plasmid DNA vaccines encoding strings of class I and II putative epitopes. In a retrospective analysis of the IFN□ responses to individual peptides compared to predictions specific to the SLA alleles of cohort pigs, we evaluated the predictive performance of PigMatrix and demonstrated its ability to distinguish non-immunogenic from immunogenic peptides. Overall, this study confirms the capacity of PigMatrix to predict immunogenic T cell epitopes and demonstrate its potential for use in the design of more broadly cross-protective influenza and other vaccines for swine.